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Molecular Breeding Of Sugarcane Using Linkage Disequilibrium Maps And Quantitative Trait Alleles

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Sugarcane breeding generally involves forms of recurrent selection using overlapping generations of parent genotypes, with the number of parents used in the order of 100 to 400, depending on the size of the breeding program. Genetic maps of one or a few genotypes are thus not very useful in routine breeding applications, as they provide no information on the allelic variation at important loci within the breeding population. In order to integrate mapping, marker discovery and conventional breeding we have developed methods (i) to create population-level maps of haplotypes in linkage disequilibrium within the breeding population, (ii) to identify potentially useful quantitative trait alleles (QTAs) through association analysis, and (iii) to predict to performance of progeny of bi-parental crosses from the marker (QTA) profile of the parents. The usefulness of the approach has been empirically verified in an experiment which demonstrated that the performance of progeny is better predicted by parental QTAs than by parent phenotype (h2 = 0.82, versus 0.57). By examining the population-level haplotype map, cryptic population structure caused by the complex linkage arrangements that can exist in polyploids could be detected, and accounting for this structure/ linkage can further improve the effectiveness of molecular breeding. Additional uses of the map, such as identifying the ancestral origins of haplotypes, and detecting signatures of selection and recombination over several generations of breeding will be demonstrated.